100.0 148068 1 AB001488 AB001488 100.0 24907 1 AB002668 AB002668 100.0 24907 1 AB002668 AB002668	100.0 1950 1 ABO08139 ABO08139 ABO08139 100.0 1950 1 ABO08153 ABO08159 ABO08159 ABO08158	100.0 15295 1 AB010150 AB010150 100.0 2748 1 ACCPSXM X81320 A 100.0 2878 1 ACIMPDEH X66859 A 100.0 14801 1 AE000688 AE000688	100.0 15304 1 AE000692 AE000692 100.0 14150 1 AE000697 AE000697 100.0 15467 1 AE000723 AE000723 100.0 16071 1 AE000796 AE000796	100.0 10932 1 AE000801 AE000801 100.0 12282 1 AE000818 AE000818 100.0 12282 1 AE000818	100.0 10865 1 AE000838 AE000838	9 100.0 11069 1 AE000850 AE000850 Methanoba 9 100.0 9938 1 AE000870 AE000870 Methanoba 9 100.0 9938 1 AE000874 AE000874 Methanoba 9 100.0 11565 1 AE000898 AE0008974 Methanoba 9 100.0 10949 1 AE000898 AE000899 AE000898 Methanoba	100.0 10524 1 AE000906 AE000902 100.0 12634 1 AE000912 AE0009012 100.0 10575 1 AE000917	100.0 1508 1 AE000940 AE000940 100.0 20434 1 AE000954 AE000953 100.0 22014 1 AE000963 AE000963	100.0 12154 1 AE000973 AE000973 100.0 15528 1 AE001011 AE001011 100.0 11103 1 AE001052 AE001052	100.0 1703 1 AE00105/ AE00105/ 100.0 11703 1 AE001107/ 100.0 14039 1 AE001107 AE001107/ 100.0 3387 1 AF006594 AF006594	100.0 220060 1 AF008220 AF008220 100.0 220060 1 AF008220 AF008220 100.0 2374 1 AF015255 AF015255	100.0 21205 1 AF025396 100.0 21205 1 AF025396 100.0 367 43 G41695	ALIGNMENTS	AB001488 148068 bp DNA BCT 21-OCT-1	Detween 35 and 4' AB001488	; ddlA; dinB; exp2; gsiB; mutT; nap; orfR; orfS; ov V; rsbW; rsbX; sigB; topB; ydaA; ydaB; ydaC; ydaD;	G; ydaH; ydaI; ydaY; ydaL; ydaM; ydaN; ydaO; R; ydaS; ydaT; ydbA; ydbB; ydbC; ydbD; ydbE; ydbF; ydbY; ydbY; ydbC; ydbP; ydbO; ydbY; ydbO; ydbP; ydbO; ydbY; ydbO;	ydcy; ydck; ydck; ydck; ydcy; ydc; ydc; ydc; ydc; ydc; ydc; yd	o; ydep; ydeg; ydex; ydes; ydex; ydfb; ydfb; ydfc; F; ydfg; ydff; ydff; ydfx; ydfk; ydfk; ydfw; ydfw;	YdrB: ydrC; ydrR: ydfS; ydfT; ydgA; ydgB: ydgC; ydgD; ydgE; ydgG: ydgH: ydgT: ydgT: ydgX. Bacillus subtilis (strain:168) DNA. Bacillus subtilis
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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: June 24, 1999, 00:40:12; Search time 366.45 Seconds (without alignments) 87.864 Million cell updates/sec	Title: US-09-205-015-1 Perfect score: 9 Sequence: 1 tctgagtca 9	Scoring table: IDENTITY_NUC	Searched: 808301 seqs, 1788773984 residues	.	5: gb_ov:* 6: gb_pat:* 7: gb_ph:* 8: gb_pli:*	9: gb_pl2:* 10: gb_pr1:* 11: gb_pr2:*	12: 90_ros. 12: 90_ros. 14: 90_st:* 15: 90_sy:*	16: gb_un:* 17: gb_vi:* 18: gb_htg:* 10: gb_htg:*		23: em_in:* 24: em_om:* 25: em_or:* 26: em_or:*	28: em_ph:* 29: em_ph:* 30: em_ro:*	31: em_sy:* 32: em_un:* 33: em_ui:* 34: em_thg:*			41: 9D_PT2:* 42: 9D_PT3:* 43: 9D_Sts:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Result Query No. Score Match Length DB ID Description

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EBEFCNEAVEKTVRELGGIDIUVNAGAGHPKRESIKDITGSGLHRTFKRNFYSQFYLT
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                                                                                                                                                                                                                                                                                             'note-"FUNCTION UNKNOWN, SIMILAR PRODUCT IN SEVERAL
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TERMINATOR"
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Submitted (03-MAR-1997) to the DDBJ/EMBL/GenBank databases. Naotake Submitted (03-MAR-1997) to the DDBJ/EMBL/GenBank databases. Naotake Ogasawara, Nara Institute of Science and Technology, Graduate School of Biological Sciences; 8916-5 Takayama-cho, Ikoma, Nara 630-01, Japan (E-mail:nogasawa@bs.aist-nara.ac.jp, Tel:07437-2-5430; Ex:07437-2-5439)
1. 148068
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                                                                                                                                                                                                                                                                                                                                                                                        Kasahara,Y., Nakai,S., Lee,S., Sadaie,Y. and Ogasawara,N. A 148 kbp sequence of the region between 35 and 47 degree of the
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FERMINATOR"
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Unpublished (1997)
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LFVINMLITSIYTIGVLSALXAGLLAPERSTTAVMASGLINGIATMLLAIFVDPKVSV
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responsive regulator."
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11987. .13091
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KPVSIGLWIQGELVITATDLAEFIGAALGEVILFGIPMLEASITAALGANLEEVAKEEFF
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GSLINAKWITVVSWLIAVLIVALNVELIVDTFR"
COMPLEMENT (25484. .25490)
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                                                                                                                       'note-"SIMILAR TO PYRUVATE OXIDASE AND ACETOLACIATE
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                                                                                                                                                                       SYNTHASE.
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                                                CDS
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                                 TERMINATOR
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CDS

RBS

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39362. 39386
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gene

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LARLEKDGINSPMLKDALNEGNEDLSKRAPILGDKKDESARTDQKETVEGLLKQPNNQ
QQTDDASLQBEEESTSNRAPYLQENEKDTERTPQKATITDEQNONLETDQQODFEVQK
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SEPAKVHSDGIRVDERKQAVAPAENKTVSREKQPSSQTIKRTEQSVNSFDQVSLNEIAR
RSSSKVEDRLRRDERRT"
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                                                                                                                 /gene="yddE"
/note="%IMILAR TO ORF16 OF ENTEROCOCCUS FAECALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="SIMILAR TO ORF14 OF ENTEROCOCCUS FAECALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "note-"FUNCTION UNKNOWN."
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                                                                                                                                                                                           TRANSPOSON TN916."
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FIKLPQKKYCNDRKIDLSNEKQIFFRLVKVVDYSNETKNAYEGNIQDFAVNKNGRRY
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KYASEKKEEMVYMMKKPEALEGNLLFGEVQSVKIFETKKGFEVFCAVRFKEKENDIPV
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LSGFINEYMNVKNDQESIEKRMQSLESYMVKOEDNHFEDERRNVDGLKGDRELKGYS
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TRANSPOSON TN916."
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71951. 71959
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CDS

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/gene="yddN"
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THVPYFVLGSSTDSABIAAKLGLPYAFGAOFSPHSMEBALSIYRENFOPSSYLOEPYV
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RIGYTIMGDRETIRRELIDFOQMYHADELIVLSNIYELSKEIQSYEILKQVVDELFKK
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ADVENFSIEVADYFHEQGNIMISNEYYRMSIEARRKIKKGEIIDENQPDSIGSSDFK"
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REGULATORY PROTEIN ASNC."
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                                                                                                                                                                                 TERMINATOR"
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complement(93838. 93846)
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94365. 94393
TEMINATOR"
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95707, .95714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"PROBABLE TRANSCRIPTIONAL REGULATOR, SIMILAR TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="SIMILAR TO YOFU, YXKD, YITB OF B. SUBTILIS."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /octe-"FUNCTION UNKNOWN, SIMILAR PRODUCT IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="PROBABLE NAD(P)H OXIDOREDUCTASE."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(108930. .109358)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(115754. .116674)

complement(115754. .116674)

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A-RESISTANCE GENE."
A-COOD_STANTE GENE."
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                                                                               'gene="ydfB'
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IKRQFSDVEEVLIHVNPFFEE"
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                                                                                                                                             'note-"FUNCTION UNKNOWN, SIMILAR PRODUCT IN SYNECHOCYSTIS
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130332, 131
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                                                                                                                                                                                                  E. COLI."
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IAVNQEQRLPIELIMDGEIIENNLKQNRLTESWLLEELRRDIKVKETVYAVLLGNGD
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                                                                                                                                                                                                                                                                                                                       'note-"SIMILAR TO YDFS GENE PRODUCT OF THIS ENTRY
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TERMINATOR"
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134222. .134
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145272. . . 145297
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LVAARFLQGFTASAGLVLSRAIVRDVFTGRELSKFFSLLAVITAVAPMYAPMTGGAIL
LLPFATWHTIFHVLMIIGFLLVLIALRLKFTLPLEKRIPSSIGTSVKTMGSLLKDRS
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REQUIRED FOR SURVIVAL IN MACROPHAGE."
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28420 c 32882 g 41602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TERMINATOR"
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ORIGIN
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LEFTAAQWTEPIKHMSMGERVKIKLAAXILEERDVLILDEPRHLDLPSREQLEETLS
QYSGTLLAYSHDRYELEKTINSKLYISNNGTEKQLNDVPSERNEREEIRLKLETERQE
VLGKLSFMTPNDKGYKELDQARNELIKRIKELDHQDKKD

COMPLEMENT (139604. .139613)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="PID: 91881370"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="PROBABLE TRANSPORT PROTEIN, SIMILAR PRODUCT IN
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TERMINATOR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(141303. .141308)
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complement(141465. .142000)
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complement(139917. .141293)
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NRKWHSRVLDGSYNERLGSQ"
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10090. .10968
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Identification of a genetic locus essential for serotype b-specific antigen synthesis in Actinobacilius actinomycetemcomitans
Infect. Immun. 66 (1), 107-114 (1998)
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LEMPTLKQF I SGDGLYMTGQTEVGRYYGHTDSGFLRQ ILYGGVTYALVCFLYTFYFVR
KVA I NWFDGSWK FMLSAFV I LAACNVKADTFAFPG IMFVMLMFFSLFGSHGKQLVLFK
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                                                                                                                          Gaps
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     Length 148068;
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           DB 1; Le
3.4e+03;
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Pred. No.
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/transl_table=11
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                                                       Similarity 100:9; .Conservative
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Direct Submission
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Yoshida,Y.,
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Query Match
Best Local S
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MEDLINE
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TITLE
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XAEWRLFKLKHHLGIQGFLSGLFTFVLRSGARLLPTSLLKNIYQTFLRK**
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WAGMGOTOFRPSYLLSYADONNOGENIWTDHYDYFASIANYLHYVGWNENLEWGY
BYALTOPLDWALAGTEENKRRSLSDWONMGYTLKYOTPOTOOKLTALSGAODLWLYNF
DRELGRAFLYSNNYRTLLHWNKSNYFAVSIGMFADRIEORVK"
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IDYIRBERYKVPPQAARNFKINASYILAYPHINNLSRKAAKYYFDIFKQTRSLKQLIIA
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LLFETQFKLNNNVYRPLAVIENPQLYSNLEAVRGSKSNNLAKKLLKYPLKKLLAVKKN
                        Submitted (07-APR-1997) to the DDBJ/EMBL/GenBank databases. Yasuo yoshida, Kyushu University Faculty of Dentistry, Department of Preventive Dentistry, 3-1-1 Maidashi, Higashi-ku, Fukuoka, Fukuoka 812-82, Japan (E-mail:yasuodha@mbox.nc.kyushu-u.ac.jp, Tel:092-642-642-632, Fax:092-642-6354)

1. 24907
                                                                                                                                                                                                                                                                                                           /organism="Actinobacillus actinomycetemcomitans'
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24126. .24668
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Yoshida,Y., Nakano,Y., Yamashita,Y. and Koga,T.
Identification of a genetic locus essential for serotype b-specific antigen synthesis in Actinobacillus actinomycetemcomitans infect. Immun. 66 (1), 107-114 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                              DIVDHIGSTHVNHFGQKGHYGVALLSKQVPLSYRKGFPTDDEEAQKRIIMIDLETKFGQ
LTVINGYFPQGESREHPTKFPAKQKFYADLQRYLEQDHNAQNPVIIMGDMNISPSDLD
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23307. .24101
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YYEMVRPGLSGLWQVSGRNDIGYATRVYLDAMYVKNWSLMNDIVILAKIVNIVLRRKG
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Actinobacillus.
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Yoshida, Y.
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3342 TCTGAGTCA 3350
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Best Local Similarity
Matches 9; Conserv
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| 17293. .17661 | Cotton product | Codon_start | 17293. .17661 | Cotton_start | Codon_start | Codon_
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PYLLILSLPMTMFQMGSTNPDSIIFSLSVFIGSLLARGLDSNYNFTHKDFCKLLFSIF
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SLLAY FELFIHMLYKLKYVIGSYLLYGYVFEFFILLTYNBIGTTOLYGYOGRYFI
PIMLIFSSFILKKSEKTSNNKTISKYFIIVPFLFFILLTYNBIGTTOLYGYOGRYFI
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CKPFSFSYDRELYGIHKRNEPSKKHIFFYARPPTERRAFELGLLVLDKVTKKRPDISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFAGWDVSSYEIPFHHLNAGIVKLDELSNLYSQCDAALVLSFTNLSLLPLELLASGCP
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                                                                                                                                                                                                                                                                                            KKEKLYWSYFSLIKNTVKYTGAYFGPKGTNNKLITKLFSRELILRNK
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18374. .18754
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1 4293 c 5099 g 7976 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochemical and molecular characterization of the polyhydroxybutyrate depolymerase of Comamonas acidovorans YM1609, isolated from freshwater Appl. Environ. Microbiol. 63 (12), 4844-4852 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AB003186 1907 bp DNA BCT 21-FEB-1998 Comamonas acidovorans gene for polyhydroxybutyrate depolymerase,
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100.0%; Score 9; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 9; Conservative 0; Mismatches 0;
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119. .1603
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TITLE
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SOURCE
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Direct Submission
Submitted (15-OCT-1997) to the DDBJ/EMBL/GenBank databases. Hosami Harada, Graduate School of Science, University of Tokyo, Department of Biological Sciences; Hongo, Bunkyo-ku, Tokyo 113, Japan (B-mail:hosami@biol.s.u-tokyo.ac.jp, Bunkyo-ku, Tokyo 113, Japan (B-mail:hosami@biol.s.u-tokyo.ac.jp, Tel:03-3812-2111, Fax:03-3816-1965)

Tel:03-812-2111, Fax:03-3816-1965)

Cocation/Qualifiers

.. 1950
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Hardda,H. and Ishikawa,H.
Phylogenetical relationship based on groE genes among
phenotypically related Enterobacter, Pantoea, Klebsiella, Serratia,
and Erwinia species
J. Gen. Appl. Microbiol. 43, 355-361 (1997)
                                                                                                                                                                                                                   DNA BCT 21-MAR-1998 for GroES protein homologue, GroEL protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GroES protein homolog; GroEL protein homolog.
Erwinia aphidicola (strain:IAM14479) DNA.
Erwinia aphidicola
Eubacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae;
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1larity 100.0%; Pred. No. 6.4e+03;
Conservative 0; Mismatches 0;
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Erwinia aphidicola gene
homologue, partial cds.
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1356 TCTGAGTCA 1348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harada, H. and Ishikawa, H.
Phylogenetical relationship based on groE genes among
phenotypically related Enterobacter, Pantoea, Klebsiella, Serratia,
and Erwinia species
J. Gen. Appl. Microbiol. 43, 355-361 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GroES protein homolog; GroEL protein homolog.

Briterobacter gergoviae (strain:JCM 1234) DNA.

Enterobacter gergoviae

Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                   AB008139 1933 bp DNA BCT 21-MAR-1998
Enterobacter gergoviae gene for GroES protein homologue, GroEL
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    1933
    Organism="Enterobacter gergoviae" /strain="UCM 1234" /db_xref="taxon:61647"

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Matches 9; Conserv
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Gaps

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BASE COUNT ORIGIN

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FEATURES

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5406. 6620
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5406. 6620
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4612. .5406
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                                                                                                                                                                                 mannosyltransferase; ATP binding component of ABC-transporter;
phosphomannomutase; GDP-mannose pyrophosphorylase;
gluconate-6-phosphate dehydrogenase; integral membrane component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (07-JAN-1998) to the DDBJ/EMBL/GenBank databases.
TSuyoshi Sugiyama, Alchi Medical University, Department of
Microbiology and Immunology; Yazako, Nagakute, Alchi 480-11, Japan
(E-mail:sugiyama@aichi-med-u.ac.jp, Tel:0561-62-3311,
                                                                                                                                                                                                                                                                                         Escherichia coli (strain:F492) DNA, clone_lib:31 clone:pTSO8.
Escherichia coli
Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sugiyama,T., Kido,N., Kato,Y., Kolde,N., Yoshida,T. and Yokochi,T. Generation of escherichia coli O9a serotype, a subtype of E. coli O9, by transfer of the wb* gene cluster of klebsiella O3 into E. coli via recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sugiyama, T., Kido, N., Koide, N., Kato, Y., Yoshida, T., Jiang, G., Paeng, N., Takahashi, K., Morikawa, A. and Yokochi, T.
Nucleotide sequence of Escherichia coli 08 wb gene cluster
Unpublished (1998)
3 (bases 1 to 15295)
                                                                            21-MAY-1998
                                          AB010150 15295 bp DNA BCT .
Escherichia coli O8 wb gene cluster, complete cds.
AB010150
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1. .15295
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44. 49
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/note="putative"
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/note="putative"
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/transl_table=11
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1722. 1777
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'note="putative"
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146. .1552
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146. .1552
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                                                                                        DEFINITION
ACCESSION
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RESULT
AB010150
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11579. .11582
13886. .13906
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281. .1088
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291. .1088
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1 (bases 1 to 2748)
Stark,M. and Kaplan,N.
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Best Local Similarity 100.
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complement(lil6. 2545)
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Submitted (06-SEP-1994) M. Stark, Tel Aviv University, Dept of
Molecular Microbiology & Biotechnology, Ramat-Aviv, 69978 Tel-Aviv,
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                                                                                                                                                                                                                 Gaps
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Eubacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epsM; epsX; GDP-mannose pyrophosphorylase; phosphomannose
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                                                                                                                                                    Length 15295;
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1. .2748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCT
                                                                                                                                              100.0%; Score 9; DB 1; Le
100.0%; Pred. No. 4.8e+03;
1ve 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCPSXM 2748 bp DNA A.calcoaceticus epsX and epsM genes. X81320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative indicates no similarity to known proteins Hypothetical indicates similarity to a protein of unknown function. Location Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deckert, G., Warren, P.V., Gaasterland, T., Young, W.G., Lenox, A.L.,
Deckert, G., Warren, P.V., Gaasterland, T., Young, W.G., Lenox, A.L.,
Graham, D.E., Overbeek, R., Snead, M.A., Keller, M., Aujay, M.,
Huber, K., Feldman, R.A., Short, J.M., Olson, G.J. and Swanson, R.V.
Direct Submission
Submitted (25-JUL-1997) Diversa Corporation, Genomics, San Diego,
                                                                                                                                                                                                                                                                                                                                                                          Eubacteria; Aquificales; Aquificaceae; Aquifex.

[ bases 1 to 14801)

Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.,
Graham,D.E., Overbeek,R., Short,J.M., Clson,G.J. and Swanson,R.V.

Huber,R., Feldman,R., Short,J.M., Olson,G.J. and Swanson,R.V.

The complete genome of the hyperthermophilic bacterium Aquifex
                                    Gaps
                                                                                                                                                                                        AEUU0688 14801 bp DNA BCT 30-OCT-1
Aquifex aeolicus section 20 of 109 of the complete genome.
AE000688 AE000657
92983063
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                                    Indels
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           Pred. No. 6.1e+03; 
; Mismatches 0;
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9; Conservative 0
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                                                                                                   Best Local Similarity
Matches 9; Conserv
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AE000688/c
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AUTHORS
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SIQMHHHRSEHWIVVNGTAKIHKGKESFLLTENQSTYIPLGEIHALENPGKVPLELIE
VQSGSYLGEDDIVRFEDLYGRC"
complement(2541. .2545)
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505 c 681 g 838 L
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A calcoaceticus gene for inosin-5-monophosphate dehydrogenase and
putative feredoxin.
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eubacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
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Submitted (11.JUN-1992) U. Anderegg, Univ. Leipzig, Fach.
Blowissenschaften, Talstrase 33, 0-7010 Leipzig, FRG
2 (bases 1 to 2878)
Anderegg, U., Schunck, W.H., Asperger, O. and Kleber, H.P.
Unpublished
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                                                                                                                                                                             B 1; Length 2748; .2e+03; s 0; Indels
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    .2878
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                                                                                          901
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Acinetobacter calcoaceticus
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SEKERIADIIETDVGIAVKFYLOFWORSFYFARKKIESLEHAVSFVGWBNKKFYLIVS
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LRELNVDEEVVKAFEDKGSSLHKLLEVVSRLEBAVNSSPEELDKTAQOLSOELGIPEI
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pkilfvneknopvevkestevk"
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Hypothetical indicates similarity to a protein of unknown function.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-JUL-1997) Diversa Corporation, Genomics, San Diego,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.,
Graham,D.B., Overbeek,R., Snead,M.A., Keller,M., Aujay,M.,
Huber,K., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deckert, G., Warren, P.V., Gaasterland, T., Young, W.G., Lenox, A.L. Graham, D.E., Overbeek, R., Snead, M.A., Keller, M., Aujay, M., Huber, R., Feldman, R.A., Short, J.M., Olson, G.J. and Swanson, R.V. The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                 30-0CT-1997
                                                                                                                      AE000692 15304 bp DNA BCT 30-OCT-1
AE011fex aeclicus section 24 of 109 of the complete genome.
AE000692 AE000657
92983130
                                                                                                                                                                                                                                                                                                         Aquifex aeolicus.
Aquifex aeolicus
Eubacteria, Aquificales; Aquificaceae; Aquifex.
L (bases 1 to 15304)
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    15304
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/strain="VF5"

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98196666
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403. .777
/note="aq_476"
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                                                                                                                                                        DEFINITION
ACCESSION
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                                                 RESULT 1
AE000692
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IWLTDLKNFLRRELSVKLSLYLFTLSGISFFLKALSTYILVESLVRLNLFEYTLGFL
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FRSGAPLLNMFGAKIGVGFWTLIPRDVEVFWVDVFDDVDKGIDWADVVIWLRLQKER
CKENTIPESSYFKQFGLTKERFEKVKLYMHPGPVNRNVDIDHELVYTEKSLIQEGVK
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/db_xref-*putative protein"
/db_xref-*putatio-*putative
/db_xref-*putatio-*mplanty
/translatio-*mplanty
/tr
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KENNVYGIVGTEDTRALVKRIERKGSMRGVISTVERDEKKLVOKARELEDDISEQALVEE
VSAKDIYYMNGGYDDPRGFELYRENBKPLVAYIDFGVKFNILRRLYSEGAKVVVVPPP
NAKEAIEKINPDAIFLSNGPGDPERVISGIRLTREYMEKKPIKGICLGCQIIGLALGG
KTYKLKFGHHGGNHPVKDLRTGKIEITAQNHNRAIDPESLPEDVEVTHLNLLDNTVEG
KTHKHLDAVQYHERNSPGPDSYXLFKEFVKMAQG"
3311 c 3301 g 3744 t
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/db_xref="PID:92983067"
/translation="MRKTAILALEDGSYFYGYSFGAEGETGGELVFNTSWTGYQEILT
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                                                                                                                                                                                                                 complement(11333. .11944)
/gene="aq_407"
complement(11333. .11944)
/gene="aq_407"
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/note="aq_410"
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Best Local Similarity
Matches 9; Conserv
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ADLESGRGTGRLLEDELYBNVOGYRALGRAGKVVEKTOLYIGENGERSKYTEDKIL

ILSVRLVPDENDKYYLLEVVGSRGRYVKERZIGENGERVPKEKTOLYIGERGESK

TLILLEGGLKENTGGYGADYYIKBEYLLEDKEVVKEKFPLEGGIGVPIR"

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Gomplement(10500. .11261)

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/gene"aq_494"
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AGEAFIAPIEESAFGKLVILYAPNRKLEREITLYFKDGAVERIEGFEDYRYELERVFD
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//Laneiation-"pi19298143"
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IKNVKTVSDTDKLIASLTQTABEFKRYAQNINTILLENRENLRQTIAHLNYLININE
ITEONRGKHKLSSEEFKIIDRIFKQGSARSPRYFE"
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complement(8619. .9557)
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complement(7799. .8521)
                                                                                             complement(7799.
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REKPKKFLSEKPIKIKIKARALVEVEKSLLRELGISWRTVFSKAYIPEFWGETAFRIV
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Hypothetical indicates similarity to a protein of unknown function
Local protein of a protein of unknown function and the second seco
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Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.,
Graham,D.B., Overbeek,R., Snead,M.A., Keller,M., Aujay,M.,
Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.
Direct Submission
                                                                                         Aquifex aeolicus
Eubacteria; Aquificales; Aquificaceae; Aquifex.

1 (bases 1 to 14150)

Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.,

Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aujay,M.,

Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.

The complete genome of the hyperthermophilic bacterium Aquifex
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REFERENCE
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KEYWORDS
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Aquifex aeolicus section 29 of 109 of the complete genome.
AE000697 AE000657
g2983212
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/db_xref="PID:92983136"
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complement(14434. .15234)
/gene="aq_499"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(13532, .14434)
/note="aq_498"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLFKNKVLAVLRYEFGRHRVKKKD" complement(14434. .15234)
                                                                                                                                                                                                                                                                                                                                                                                                                      complement(12274. .13569)
/note="aq_497"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(12274. .13569)
/gene="gsdA"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                        DLCEYGOKNLKGRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="gsdA"
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RLEELKELLKRRFLRTGRR"
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KGFLSKSVERISDVLRCSVEELEKVRQKVLRLEPLGVCSKDVWEFLELQIEETYPEE
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YLYEDFIDIDLNEFYWETKGRNLQKELKEAFERYESIRKVLDIRRRNLRKVLEKIY
ERQKDFLTGKGSLKPTLRKFVSSEIGHESTLSRIVNSKYVKYPOGTYSLKTFYRSA
AEGLTGGELMKLIKEIVENDERKRFYSDQEIANILKEKGFKVARRTVAKYREMIGIPS
                                                                                                                                              SERICGLARVIRANSIPAMEDVVLMHERDISHSVERVILPDSFIALDYILNEYEIL
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                                       TALALLIREAIDIILKDIDKVMEEIKRLAFEHKDTLMMGRTHGVHAEPYTFGLKMCVW
YDEMRRQKERLLFARENVLYGKISGAVGTYSNIPPEVEKLALEELGLKIEPASTQIVH
RDRHAQLLTTLGLIASSLEKFATEIRHLQRTEVLEVLEPFTKGQRGSSAMPHKKNPIH
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           JKKIEEKTYVDKKVVEKIKEKEKVFKHDVLAFVSVIAEQVGEEGRYIHMGLTSSDVVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLYQADEFKELAEEVENTIKKIMEEAAK"
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/gene="aq_600"
complement(12640. .13122)
                                                                                                                                                                                                                                                                                                                                                (10935, .11327)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative
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/transl_table=11
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/transl_table=11
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/gene="aq_601"
13479. .14015
/gene="aq_601"
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                                                                                                                                                                                                                                                                                                                                                                                    /gene="aq_598"
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/gene="rpoN"
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REVYYWSLKDKEKYKETYENLKKGSIPSGYTERDRDPPFKYKEAVKELNOENRIKVY
RVGENYYLLYYGKENAGY RPLEEVKEEIKRELVAKKOREKLKEFAGEVFKNLKEGKE
VGYRPLAFSSASLEEICRILMYECKLIKPKYFYERYYGPYPSLAGYGILVVKNRKFE
ELKPEQVKEIERELKDILMYECKLIKEYGYTVOORDAGI"
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EERKY "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="PID:g2983218"
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REAELLKEAQYAWNTGDFYRAHEILEEVWGLFKNEEIKKCYRGLIRAAIALHRFKEGN
PQSGANVVKQALLDWANCPDNFRGINLGEIRAYLEEVLGTKEIGNPFELKYNIKSEE"
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DEEVVEVIKNDENFKEKGKFSVEKYRETLNRFGLTPAEYEEIVRKSLMAQRVLNFLRE
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VLIGDVKAMDTECSILLSGOKNLIGALGEDYVOTGEDENTLIVKRNSYGKVKRIVK
ELEEENDERAIEHVYSTPFGSITKLDRGERKIRKVVKKDREIDLAMHHHRYVHFV
VLKGTAKVKVGDKEEFVHENESFFVPKSTPYKIINVGKIPLEMIEVQSGEYLGEDDVE
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GKLEEGVYEIEKFEEKPDYEKAKEYVSDGKHFWNCGIFLFTLDRIVKDYTQLMPEIPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anticodon=(pos:6196. .6198, aa:1le)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product-"putative protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(9580. .10893)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(9580. .10893)
/note="aq_597"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(7569. .9284)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="frdA"
complement(7569. .9284)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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6259. ,7572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="frdA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
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RESULT

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//broduct="ABC transporter (hlyB subfamily)"
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GSILLGRILGPIDTIVNGWRQIGNTKVAYTRANBELKFLRFRREVSYKLEPERKGELEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAFRNNTPVIARDIKVFREIAGDNAFFFENTKNPEVIANAIKTWLELYRKGLHPKPAN
LKOYKYTWENHCKLLIKYLTEI"
5552. .7246
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FDVIVCDGFVGNVILKASESLGLAVVQMIKEEIKRSILAKLGALLLMPALNRFKKKAD
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VLEKAGVKPEEVSLVIPHQANVRIINALAEKLNIPKEKVFVNIQKYGNTSAASIPIAL
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                                                                                                                                                                                                                                                                                                                                 complement(3522. .5288)
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/note="aq_1099"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="fabH"
complement(7243. .8172)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(8173. .9186)
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                                                                                                                                                                                                                                                                                                  /gene-"mtfA
                                                                                                                                                                                                                          gene
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LKRRISTEVBLLYFKKLEMOFRYERCKOFTRYRKFFERNPFLLSLOFFL
EYSYANLIKELSKKSVENTVNDIKLAGOYERNAYEWKRRFERWPRLJCHSTYLSST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative indicates no similarity to known proteins Hypothetical indicates similarity to a protein of unknown function. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             Deckert, G., Warren, P.V., Gaasterland, T., Young, W.G., Lenox, A.L., Graham, D.E., Overbeek, R., Snead, M.A., Keller, M., Aujay, M., Huber, R., Feldman, R.A., Short, J.M., Olson, G.J. and Swanson, R.V. The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 15467)
Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.,
Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aujay,M.,
Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (25-JUL-1997) Diversa Corporation, Genomics, San Diego
                                                               30-0CT-1997
Aquifex aeolicus section 55 of 109 of the complete genome. 92983569
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                                                                                                                                                                                                                                          Aquifex aeolicus.
Aquifex aeolicus
Eubacteria: Aquificales; Aquificaceae; Aquifex.
(bases 1 to 15467)

    11. .15467
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    /strain="VF5"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 392 (6674), 353-358 (1998)
98196666
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103. .1380
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                                                                                   DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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REFERENCE
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JOURNAL
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               AE000723
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gene

CDS

CDS

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128 c 3128 c 326 g 4517 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLKEIGELCKKYEVPFVVFVDPIALSILKPPAEFGADIVVGEGQOMGIPLSFGGPYVG
PSPTKKEHVFKMPGRLVGMGEDIEGKRAFILVLGYREOHIREREATSNTCTNQNLMAL
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IYRKLLKEKIVLGLPLDRFYEDLKNTTLIAVTEKRTKEEIDSVLALL
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Smith.D.R., Doughery,C., Lee,H.-M.,
Duboit,J., Aldredge,T., Bashizadeh,R., Blakely,D., Cook,R.,
Gilbert,J., Harrison,D., Hoang,L., Keagle,P., Lumm,W., Pothier,B.,
Gilbort,J., Spadafora,R., Vicare,R., Wang,Y., Wierzbowski,J.,
Gibson,R., Jiwani,N., Caruso,A., Bush,D., Safer,H., Pathwell,D.,
Prabhakar,S., McDougall,S., Shimer,G., Goyal,A., Pietrovski,S.,
Church,G.M., Daniels,C.J., Mao,J.-i., Rice,P., Nolling,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanobacterium thermoautotrophicum
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AE000796 16071 bp DNA BCT 13-NOV-1997 Methanobacterium thermoautotrophicum from bases 10151 to 26221 (section 2 of 148) of the complete genome. AE000796 AE000666 92621057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                     /product-"glycine cleavage system protein
/db_xref-"PID:92983578"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(14874. .15329)
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                                                                                                                                                                                                                                   SEEELGYEENK
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Best Local Similarity
Matches 9; Conserv
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AE000796/c
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PFTTDRLPDLIDLRILDENPDLYJCAEVAGPENPYTEESPPYKEDVGLFVFDFMKN
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LPNLNMRFVCKWVNLRVENERSAFTRKLEKGDVLRIPIAHHDGRYYVPEEELRKMEEN
GQILFRYCDEQGEVKEEVNPNGSVSNIAGVMNKEGNVFGMMPHPERASEDILGSHDGL
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                                                                                                                                           complement(9186. .9377)
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9947. 10999
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gene

CDS

gene

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gene

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Adaxate'-"priegrotein translocase Secy"
Adaxate'-"priegrotein translocase Secy"
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4072. 4659
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VMLEIAVEKGLVENRDQMRTLPPEVQKDIQRAAKSIRERSLENNIIVDTHCTIKTPA
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similar to, pir:LN:H64359 AC:H64359, p()=5.3E-28, pid=39%"
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Ribosomal proteins; similar to, sp:LN:RL34_METJA
AC:P54053, p()=1.6E-28, pid=58%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             // years minate
// note="Function Code:12.09 - Cell Processes, Protein and
peptide secretion; similar to, sp:LN:SECY_METVA
AC:P28541, p()=5.3E-83, pid=57%"
//codo__start=1
//transl__table=11
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/transl_table=11
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4678. .5244
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/note=
                                                                                                                                                     Direct Submission
Submitted (10-AUG-1997) Genomics and Technology Development, Genome
Therapuetics Corporation, 100 Beaver Street, Waltham, MA
02154-8448, USA
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Ribosomal proteins; similar to, sp:LN:RL30_METJA
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98037514
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                                                                      2 (bases 1 to 16071)
Smith, D.R.
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CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"cytidylate kinase"
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RAQRISVRESKDIETVREEIRIRERSEAQRYREIHGIDVDDLEVYDIVINTNREDAEA
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5529. .6014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6045. .6272
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Ribosomal proteins; similar to, sp:LN:R14E_METJA
Accip54054, p()=5E-16, pid=51%"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7322. .7408
/note="87 bp direct repeat includes part of MTH33
(tRNM-Ser-1 anticodon:gga); 100% ID to interval
968101-968101-968187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7322. 7407
/note="86 bp direct repeat includes part of MTH33
(TRNA-SET-1 anticodon:gga); 88% ID to interval
967976-968061"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="86 bp direct repeat includes part of MTH33 (tRNA-Ser-1 anticodon:gga); 88% ID to interval 968061-967976"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="MIH31"
6045. .677
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/498. 7017
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/gene="MTH32"
6287. .7261
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/gene="MTH34"
7498. .7947
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/gene="MTH32"
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| inhfslrimpervilgtdydgvytrnpkkhpdarlldvigslddlessldgtlytdyg
| gwvgxtreilliaekgveseiinaavpgnierallgeevrgtritgkh"
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GWGVISELNATMCGYGPVAATIIASRILGATECDLLRYATSGDVTGDRSSVVGYAHL
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15206. .16006
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Matches 9; Conserv
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GIVGQAEAARWVIARGLVDWTSDMDLKEKFVQYDRTMLVGDPRRSEPKKYGGRGARAR
RQKSYR"
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Rlbosomal proteins; similar to, sp:LN:RL13_METJA
AC:P54023, p()-1.4E-34, pid-25%"
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Transcription--mRNA synthesis and modification (includes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10-AUG-1997) Genomics and Technology Development, Genome Therapuetics Corporation, 100 Beaver Street, Waltham, MA 02154-8448, USA
                                                                                                                                                                                                          1 (bases 1 to 10932)
Smith, D.R., Deloughery, C., Lee, H.-M.,
Dubois, J., Aldredge, T., Bashizadeh, R., Blakely, D., Cook, R.,
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                                                                                                                                 Methanobacterium thermoautotrophicum.
Methanobacterium thermoautotrophicum
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanobacterium.
            AE000801 10932 bp DNA BCT 13-NOV-1997 Methanobacterium thermoautotrophicum from bases 68653 to 79584 (section 7 of 148) of the complete genome.

92620145
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Smith, D.R.
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KEYWORDS
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CDS

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Complement(10314. 10404)

Note="91 bp direct repeat includes part of MTH123
(sensory transduction histidine kinase - paralog.fam. 1);
81% ID to interval 74/564"

Complement(10316. 10398)

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// fransl_table=11
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// franslation="whoseved protein p
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PRSYTLETLPRPLADRIRFREEKDQRRAAYRFSGRVNSDMAAQRIAELKEWLERNSIE
5187. 5930
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/product="unknown"
/product="unknown"
/product="unknown"
/product="unknown"
/translation="wornrights"
/tr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5187. .5930

5187. .5930

//gene="MTH116"

//note="Function Code:14.01 - Unknown, Conserved protein;

similar to, pir:LN:G64472 AC:G64472, p()=2.8E-22, pid=25%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7097. .7273
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7097. .7273
7097. .7273
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Matidine metabolism; similar to, gp:GI:g1001367,
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gp:61:91835286 LN:XCU70889, p()=0.99995, pid=09%"
/codon_start=1
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/gene="MTH119"
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gene

CDS

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/note="53 bp direct repeat includes part of MTH123
/sensory transduction histidine kinase - paralog.fam. 1);
87% ID to interval 408704"

10316. .10397
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/note="82 bp inverted repeat includes part of MTH123
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83% ID to interval 8984"
/note="83 bp inverted repeat includes part of MTH123
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83% ID to interval 5547"

n complement(10322. .10404)
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86% ID to interval 30584*

n complement(10346. .10396)
/note="51 bp inverted repeat includes part of MTH123
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90% ID to interval 4001"
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90% ID to interval 4001"
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/sensory transduction histidine kinase - paralog.fam. 1);
90% ID to interval 4001"
/note="51 bp inverted repeat includes part of MTH123
/sensory transduction histidine kinase - paralog.fam. 1);
90% ID to interval 4001"
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